

SEQUENCE LISTING

<110> SHIMOKAWATOKO, Yasutaka
NISHIO, Shoichi

<120> A method for evaluating the ability of a compound to inhibit the
protoporphyrinogen oxidase activity

<130> 2185-324P

<140> 09/289,180

<141> 1999-04-09

<150> JP 10/099619

<151> 1998-04-10

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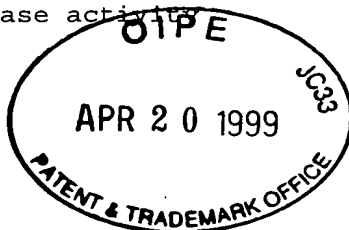
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35 40 45
Ser Asp Gly Ala Ile Phe Glu Leu Gly Pro Arg Gly Ile Arg Pro Ala
50 55 60
Gly Ala Leu Gly Ala Arg Thr Leu Leu Leu Val Ser Glu Leu Gly Leu
65 70 75 80
Glu Ser Glu Val Leu Pro Val Arg Gly Asp His Pro Ala Ala Gln Asn
85 90 95
Arg Phe Leu Tyr Val Gly Gly Ala Leu His Pro Leu Pro Ser Gly Leu
100 105 110
Arg Gly Leu Leu Arg Pro Ser Pro Pro Phe Ser Lys Pro Leu Phe Trp
115 120 125
Ala Gly Leu Arg Glu Leu Thr Lys Pro Arg Gly Lys Glu Pro Asp Glu
130 135 140
Thr Val His Ser Phe Ala Gln Arg Arg Leu Gly Pro Glu Val Ala Ser
145 150 155 160
Leu Ala Met Asp Ser Leu Cys Arg Gly Val Phe Ala Gly Asn Ser Gln
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Glu Leu Ser Ile Arg Ser Cys Phe Pro Ser Leu Phe Gln Ala Glu Gln
180 185 190
Thr His Gly Ser Met Leu Leu Gly Leu Leu Leu Gly Ala Gly Gln Thr
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Pro Gln Pro Asn Ser Ser Leu Ile Arg Gln Ala Arg Ala Glu Arg Trp
210 215 220
Ser Gln Trp Ser Leu Arg Gly Gly Leu Glu Met Leu Pro Gln Ala Leu
225 230 235 240
His Asn Tyr Leu Thr Ser Lys Gly Val Thr Ile Leu Ser Gly Gln Pro
245 250 255
Ala Cys Gly Leu Ser Leu Gln Pro Glu Gly His Trp Lys Val Ser Leu
260 265 270
Gly Asp Ser Ser Leu Glu Ala Asp His Ile Ile Ser Thr Ile Pro Ala
275 280 285



56

58

a

Ser Val Leu Ser Lys Leu Leu Pro Ala Glu Ala Ala Pro Leu Ala His
 290 295 300
 Ile Leu Ser Thr Ile Gln Ala Val Ser Val Ala Val Val Asn Leu Gln
 305 310 315 320
 Tyr Lys Gly Ala Cys Leu Pro Val Gln Gly Phe Gly His Leu Val Pro
 325 330 335
 Ser Ser Glu Asp Pro Thr Val Leu Gly Ile Val Tyr Asp Ser Val Ala
 340 345 350
 Phe Pro Glu Gln Asp Gly Asn Pro Pro Gly Leu Arg Leu Thr Val Met
 355 360 365
 Leu Gly Gly Tyr Trp Leu Gln Lys Leu Lys Ala Asn Gly His Glu Leu
 370 375 380
 Ser Pro Glu Leu Phe Gln Arg Ala Ala Gln Glu Ala Ala Ala Thr Gln
 385 390 395 400
 Leu Gly Leu Lys Glu Gln Pro Ser His Cys Leu Val His Leu His Lys
 405 410 415
 Asn Cys Ile Pro Gln Tyr Thr Leu Gly His Trp Gln Lys Leu Asp Ser
 420 425 430
 Ala Leu Gln Phe Leu Thr Ala Gln Arg Leu Pro Leu Thr Leu Ala Gly
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 CGACTTTCCC CCAGGCCTTA CG ATG GCC CGG ACT GTG ATA GTG CTT GGC GGA 172
 Met Ala Arg Thr Val Ile Val Leu Gly Gly
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 GGT ATC AGC GGA TTG GCC GCA AGT TAT CAT CTG ACC CGA AGC CCC AGT 220
 Gly Ile Ser Gly Leu Ala Ala Ser Tyr His Leu Thr Arg Ser Pro Ser
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 CCT CCT AAG GTG ATC TTA GTG GAG GGC AGC AAA CGT TTG GGA GGC TGG 268
 Pro Pro Lys Val Ile Leu Val Glu Gly Ser Lys Arg Leu Gly Gly Trp
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 ATC CGT TCA GTC CGA GGA TCA GAT GGT GCG ATC TTT GAA CTT GGA CCT 316
 Ile Arg Ser Val Arg Gly Ser Asp Gly Ala Ile Phe Glu Leu Gly Pro
 45 50 55
 CGA GGA ATT AGG CCG GCT GGA GCC CTG GGA GCC CGG ACC CTG CTC CTG 364
 Arg Gly Ile Arg Pro Ala Gly Ala Leu Gly Ala Arg Thr Leu Leu Leu
 60 65 70
 GTT TCT GAA CTT GGC TTG GAA TCC GAA GTC TTG CCT GTC CGA GGG GAT 412
 Val Ser Glu Leu Gly Leu Glu Ser Glu Val Leu Pro Val Arg Gly Asp
 75 80 85 90
 CAT CCA GCT GCC CAG AAC CGG TTC CTG TAT GTA GGC GGT GCC CTG CAC 460
 His Pro Ala Ala Gln Asn Arg Phe Leu Tyr Val Gly Gly Ala Leu His
 95 100 105
 CCC CTA CCC TCT GGC CTC AGG GGG CTA CTT CGT CCT TCA CCC CCC TTC 508
 Pro Leu Pro Ser Gly Leu Arg Gly Leu Leu Arg Pro Ser Pro Pro Phe
 110 115 120

2
 57 59

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TCA	AAA	CCT	CTA	TTT	TGG	GCT	GGA	CTG	AGG	GAG	TTG	ACG	AAG	CCC	AGG	556
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GGC	AAA	GAG	CCT	GAT	GAG	ACT	GTG	CAC	AGT	TTT	GCC	CAG	CGC	CGC	CTT	604
Gly	Lys	Glu	Pro	Asp	Glu	Thr	Val	His	Ser	Phe	Ala	Gln	Arg	Arg	Leu	
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GGA	CCT	GAG	GTG	GCG	TCT	CTG	GCT	ATG	GAC	AGC	CTT	TGC	AGA	GGA	GTG	652
Gly	Pro	Glu	Val	Ala	Ser	Leu	Ala	Met	Asp	Ser	Leu	Cys	Arg	Gly	Val	
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TTT	GCT	GGC	AAC	AGC	CAA	GAG	CTC	AGC	ATC	CGG	TCC	TGC	TTT	CCC	AGT	700
Phe	Ala	Gly	Asn	Ser	Gln	Glu	Leu	Ser	Ile	Arg	Ser	Cys	Phe	Pro	Ser	
			175						180					185		
CTC	TTC	CAA	GCT	GAA	CAA	ACC	CAC	GGG	TCC	ATG	TTA	CTG	GGG	CTG	CTG	748
Leu	Phe	Gln	Ala	Glu	Gln	Thr	His	Gly	Ser	Met	Leu	Leu	Gly	Leu	Leu	
			190					195				200				
CTG	GGG	GCA	GGG	CAA	ACT	CCA	CAG	CCC	AAT	TCC	TCA	TTA	ATT	CGT	CAG	796
Leu	Gly	Ala	Gly	Gln	Thr	Pro	Gln	Pro	Asn	Ser	Ser	Leu	Ile	Arg	Gln	
		205					210					215				
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Ala	Arg	Ala	Glu	Arg	Trp	Ser	Gln	Trp	Ser	Leu	Arg	Gly	Gly	Leu	Glu	
		220					225				230					
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Met	Leu	Pro	Gln	Ala	Leu	His	Asn	Tyr	Leu	Thr	Ser	Lys	Gly	Val	Thr	
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ATC	CTC	AGT	GGT	CAG	CCA	GCC	TGC	GGG	CTC	AGC	CTT	CAG	CCA	GAA	GGG	940
Ile	Leu	Ser	Gly	Gln	Pro	Ala	Cys	Gly	Leu	Ser	Leu	Gln	Pro	Glu	Gly	
				255				260						265		
CAC	TGG	AAG	GTG	TCT	CTA	GGG	GAC	AGC	AGT	CTG	GAG	GCT	GAC	CAC	ATT	988
His	Trp	Lys	Val	Ser	Leu	Gly	Asp	Ser	Ser	Leu	Glu	Ala	Asp	His	Ile	
			270					275					280			
ATA	AGC	ACC	ATT	CCA	GCT	TCA	GTG	CTC	AGC	AAG	CTG	CTC	CCT	GCC	GAG	1036
Ile	Ser	Thr	Ile	Pro	Ala	Ser	Val	Leu	Ser	Lys	Leu	Leu	Pro	Ala	Glu	
		285					290					295				
GCT	GCA	CCT	CTG	GCT	CAC	ATC	CTG	AGT	ACC	ATC	CAA	GCT	GTG	TCT	GTG	1084
Ala	Ala	Pro	Leu	Ala	His	Ile	Leu	Ser	Thr	Ile	Gln	Ala	Val	Ser	Val	
		300				305					310					
GCC	GTG	GTG	AAT	CTG	CAG	TAC	AAA	GGA	GCT	TGT	CTG	CCT	GTG	CAG	GGA	1132
Ala	Val	Val	Asn	Leu	Gln	Tyr	Lys	Gly	Ala	Cys	Leu	Pro	Val	Gln	Gly	
		315			320					325					330	
TTT	GGA	CAT	CTG	GTG	CCA	TCC	TCA	GAA	GAC	CCG	ACC	GTC	CTG	GGA	ATC	1180
Phe	Gly	His	Leu	Val	Pro	Ser	Ser	Glu	Asp	Pro	Thr	Val	Leu	Gly	Ile	
				335					340					345		
GTG	TAT	GAC	TCG	GTT	GCT	TTT	CCT	GAG	CAG	GAT	GGG	AAC	CCC	CCA	GGC	1228
Val	Tyr	Asp	Ser	Val	Ala	Phe	Pro	Glu	Gln	Asp	Gly	Asn	Pro	Pro	Gly	
			350					355					360			
CTC	AGA	CTG	ACT	GTG	ATG	TTG	GGA	GGT	TAC	TGG	TTA	CAG	AAG	CTG	AAA	1276
Leu	Arg	Leu	Thr	Val	Met	Leu	Gly	Gly	Tyr	Trp	Leu	Gln	Lys	Leu	Lys	
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GCC	AAT	GGC	CAT	GAA	TTG	TCT	CCA	GAG	CTA	TTC	CAA	CGA	GCA	GCA	CAG	1324
Ala	Asn	Gly	His	Glu	Leu	Ser	Pro	Glu	Leu	Phe	Gln	Arg	Ala	Ala	Gln	
		380					385				390					
GAA	GCG	GCT	GCC	ACA	CAG	TTA	GGA	CTG	AAA	GAG	CAA	CCA	AGC	CAT	TGC	1372
Glu	Ala	Ala	Ala	Thr	Gln	Leu	Gly	Leu	Lys	Glu	Gln	Pro	Ser	His	Cys	
		395			400					405					410	
TTG	GTC	CAT	CTA	CAC	AAA	AAC	TGT	ATC	CCT	CAG	TAT	ACA	CTA	GGC	CAC	1420
Leu	Val	His	Leu	His	Lys	Asn	Cys	Ile	Pro	Gln	Tyr	Thr	Leu	Gly	His	
				415					420					425		
TGG	CAA	AAA	CTA	GAC	TCA	GCT	CTG	CAA	TTC	CTG	ACG	GCC	CAG	AGG	TTG	1468
Trp	Gln	Lys	Leu	Asp	Ser	Ala	Leu	Gln	Phe	Leu	Thr	Ala	Gln	Arg	Leu	
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58 60

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Pro Leu Thr Leu Ala Gly Ala Ser Tyr Glu Gly Val Ala Val Asn Asp
445 450 455
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Cys Ile Glu Ser Gly Arg Gln Ala Ala Ile Ala Val Leu Gly Thr Glu
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TCG AAC AGC TGA CCCCCACTCT CCTACTCATG AAAGTAAAAG TTGATGGAGC 1614
Ser Asn Ser
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Thr Ala Ala Ala Arg Arg Thr Leu His Arg Thr Ala Ala Ala Ala Thr
50 55 60
Gly Ala Pro Thr Ala Ser Gly Ala Gly Val Ala Lys Thr Leu Asp Asn
65 70 75 80
Val Tyr Asp Val Ile Val Val Gly Gly Gly Leu Ser Gly Leu Val Thr
85 90 95
Gly Gln Ala Leu Ala Ala Gln His Lys Ile Gln Asn Phe Leu Val Thr
100 105 110
Glu Ala Arg Glu Arg Val Gly Gly Asn Ile Thr Ser Met Ser Gly Asp
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Gly Tyr Val Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Asn Asp Ser
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145 150 155 160
Gly Asp Pro Thr Ala Pro Arg Phe Val Trp Trp Glu Gly Lys Leu Arg
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Pro Val Pro Ser Gly Leu Asp Ala Phe Thr Phe Asp Leu Met Ser Ile
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560 62

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 245 250 255
 Arg Ile Trp Ile Leu Glu Lys Asn Gly Gly Ser Leu Val Gly Gly Ala
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 Ile Lys Leu Phe Gln Glu Arg Gln Ser Asn Pro Ala Pro Pro Arg Asp
 275 280 285
 Pro Arg Leu Pro Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg
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 Lys Gly Leu Lys Met Leu Pro Asp Ala Ile Glu Arg Asn Ile Pro Asp
 305 310 315 320
 Lys Ile Arg Val Asn Trp Lys Leu Val Ser Leu Gly Arg Glu Ala Asp
 325 330 335
 Gly Arg Tyr Gly Leu Val Tyr Asp Thr Pro Glu Gly Arg Val Lys Val
 340 345 350
 Phe Ala Arg Ala Val Ala Leu Thr Ala Pro Ser Tyr Val Val Ala Asp
 355 360 365
 Leu Val Lys Glu Gln Ala Pro Ala Ala Ala Glu Ala Leu Gly Ser Phe
 370 375 380
 Asp Tyr Pro Pro Val Gly Ala Val Thr Leu Ser Tyr Pro Leu Ser Ala
 385 390 395 400
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 Gln Leu His Pro Arg Thr Gln Gly Ile Thr Thr Leu Gly Thr Ile Tyr
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 Ser Ser Ser Leu Phe Pro Gly Arg Ala Pro Glu Gly His Met Leu Leu
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 Thr Glu Gln Leu Val Glu Gln Val Asp Lys Asp Leu Arg Asn Met Val
 465 470 475 480
 Ile Lys Pro Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val Trp
 485 490 495
 Pro Arg Ala Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu Asp
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 Lys Ala Arg Lys Ala Leu Asp Ala Ala Gly Leu Gln Gly Val His Leu
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			20					25						30		
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Arg	Pro	Thr	Pro	Phe	Ser	Val	Ala	Ser	Pro	Ala	Thr	Ala	Ala	Ser	Pro	
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GCG	ACC	GCG	GCG	GCC	CGC	CGC	ACA	CTC	CAC	CGC	ACT	GCT	GCG	GCG	GCC	190
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			50				55					60				
ACT	GGT	GCT	CCC	ACG	GCG	TCC	GGA	GCC	GGC	GTC	GCC	AAG	ACG	CTC	GAC	238
Thr	Gly	Ala	Pro	Thr	Ala	Ser	Gly	Ala	Gly	Val	Ala	Lys	Thr	Leu	Asp	
	65					70					75					
AAT	GTG	TAT	GAC	GTG	ATC	GTG	GTC	GGT	GGA	GGT	CTC	TCG	GGC	CTG	GTG	286
Asn	Val	Tyr	Asp	Val	Ile	Val	Val	Gly	Gly	Gly	Leu	Ser	Gly	Leu	Val	
	80				85					90					95	
ACC	GGC	CAG	GCC	CTG	GCG	GCT	CAG	CAC	AAA	ATT	CAG	AAC	TTC	CTT	GTT	334
Thr	Gly	Gln	Ala	Leu	Ala	Ala	Gln	His	Lys	Ile	Gln	Asn	Phe	Leu	Val	
			100						105					110		
ACG	GAG	GCT	CGC	GAG	CGC	GTC	GGC	GGC	AAC	ATT	ACG	TCC	ATG	TCG	GGC	382
Thr	Glu	Ala	Arg	Glu	Arg	Val	Gly	Gly	Asn	Ile	Thr	Ser	Met	Ser	Gly	
			115						120				125			
GAT	GGC	TAC	GTG	TGG	GAG	GAG	GGC	CCG	AAC	AGC	TTC	CAG	CCC	AAC	GAT	430
Asp	Gly	Tyr	Val	Trp	Glu	Glu	Gly	Pro	Asn	Ser	Phe	Gln	Pro	Asn	Asp	
	130						135					140				
AGC	ATG	CTG	CAG	ATT	GCG	GTG	GAC	TCT	GGC	TGC	GAG	AAG	GAC	CTT	GTG	478
Ser	Met	Leu	Gln	Ile	Ala	Val	Asp	Ser	Gly	Cys	Glu	Lys	Asp	Leu	Val	
	145					150					155					
TTC	GGT	GAC	CCC	ACG	GCT	CCC	CGC	TTC	GTG	TGG	GAG	GGC	AAG	CTG		526
Phe	Gly	Asp	Pro	Thr	Ala	Pro	Arg	Phe	Val	Trp	Trp	Glu	Gly	Lys	Leu	
	160				165					170					175	
CGC	CCC	GTG	CCC	TCG	GGC	CTG	GAC	GCC	TTC	ACC	TTC	GAC	CTC	ATG	TCC	574
Arg	Pro	Val	Pro	Ser	Gly	Leu	Asp	Ala	Phe	Thr	Phe	Asp	Leu	Met	Ser	
				180					185					190		
ATC	CCC	GGC	AAG	ATC	CGC	GCC	GGG	CTG	GGC	GCC	ATC	GGC	CTC	ATC	AAC	622
Ile	Pro	Gly	Lys	Ile	Arg	Ala	Gly	Leu	Gly	Ala	Ile	Gly	Leu	Ile	Asn	
			195					200					205			
GGA	GCC	ATG	CCC	TCC	TTC	GAG	GAG	AGT	GTG	GAG	CAG	TTC	ATC	CGC	CGC	670
Gly	Ala	Met	Pro	Ser	Phe	Glu	Glu	Ser	Val	Glu	Gln	Phe	Ile	Arg	Arg	
		210					215					220				
AAC	CTG	GGC	GAT	GAG	GTG	TTC	TTC	CGC	CTG	ATC	GAG	CCC	TTC	TGC	TCC	718
Asn	Leu	Gly	Asp	Glu	Val	Phe	Phe	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	
	225					230					235					
GGC	GTG	TAC	GCG	GGC	GAC	CCC	TCC	AAG	CTG	TCC	ATG	AAG	GCG	GCC	TTC	766
Gly	Val	Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	
	240				245					250					255	
AAC	AGG	ATC	TGG	ATT	CTG	GAG	AAG	AAC	GGC	GGC	AGC	CTG	GTG	GGA	GGT	814
Asn	Arg	Ile	Trp	Ile	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Leu	Val	Gly	Gly	
				260					265					270		
GCC	ATC	AAG	CTG	TTC	CAG	GAA	CGC	CAG	TCC	AAC	CCG	GCC	CCG	CCG	CGG	862
Ala	Ile	Lys	Leu	Phe	Gln	Glu	Arg	Gln	Ser	Asn	Pro	Ala	Pro	Pro	Arg	
			275					280					285			
GAC	CCG	CGC	CTG	CCG	CCC	AAG	CCC	AAG	GGC	CAG	ACG	GTG	GGC	TCG	TTC	910
Asp	Pro	Arg	Leu	Pro	Pro	Lys	Pro	Lys	Gly	Gln	Thr	Val	Gly	Ser	Phe	
		290					295					300				
CGC	AAG	GGC	CTG	AAG	ATG	CTG	CCG	GAC	GCC	ATT	GAG	CGC	AAC	ATC	CCC	958
Arg	Lys	Gly	Leu	Lys	Met	Leu	Pro	Asp	Ala	Ile	Glu	Arg	Asn	Ile	Pro	
	305					310					315					
GAC	AAG	ATC	CGC	GTG	AAC	TGG	AAG	CTG	GTG	TCT	CTG	GGC	CGC	GAG	GCG	1006
Asp	Lys	Ile	Arg	Val	Asn	Trp	Lys	Leu	Val	Ser	Leu	Gly	Arg	Glu	Ala	
	320				325					330					335	
GAC	GGG	CGG	TAC	GGG	CTG	GTG	TAC	GAC	ACG	CCC	GAG	GGC	CGT	GTC	AAG	1054

62 64

2

Asp	Gly	Arg	Tyr	Gly	Leu	Val	Tyr	Asp	Thr	Pro	Glu	Gly	Arg	Val	Lys	
				340					345					350		
GTG	TTT	GCC	CGC	GCC	GTG	GCT	CTG	ACC	GCG	CCC	AGC	TAC	GTG	GTG	GCG	1102
Val	Phe	Ala	Arg	Ala	Val	Ala	Leu	Thr	Ala	Pro	Ser	Tyr	Val	Val	Ala	
				355					360					365		
GAC	CTG	GTC	AAG	GAG	CAG	GCG	CCC	GCC	GCC	GCC	GAG	GCC	CTG	GGC	TCC	1150
Asp	Leu	Val	Lys	Glu	Gln	Ala	Pro	Ala	Ala	Ala	Glu	Ala	Leu	Gly	Ser	
				370					375					380		
TTC	GAC	TAC	CCG	CCG	GTG	GGC	GCC	GTG	ACG	CTG	TCG	TAC	CCG	CTG	AGC	1198
Phe	Asp	Tyr	Pro	Pro	Val	Gly	Ala	Val	Thr	Leu	Ser	Tyr	Pro	Leu	Ser	
				385					390					395		
GCC	GTG	CGG	GAG	GAG	CGC	AAG	GCC	TCG	GAC	GGG	TCC	GTG	CCG	GGC	TTC	1246
Ala	Val	Arg	Glu	Glu	Arg	Lys	Ala	Ser	Asp	Gly	Ser	Val	Pro	Gly	Phe	
						405				410					415	
GGT	CAG	CTG	CAC	CCG	CGC	ACG	CAG	GGC	ATC	ACC	ACT	CTG	GGC	ACC	ATC	1294
Gly	Gln	Leu	His	Pro	Arg	Thr	Gln	Gly	Ile	Thr	Thr	Leu	Gly	Thr	Ile	
				420					425					430		
TAC	AGC	TCC	AGC	CTG	TTC	CCC	GGC	CGC	GCG	CCC	GAG	GGC	CAC	ATG	CTG	1342
Tyr	Ser	Ser	Ser	Leu	Phe	Pro	Gly	Arg	Ala	Pro	Glu	Gly	His	Met	Leu	
				435					440					445		
CTG	CTC	AAC	TAC	ATC	GGC	GGC	ACC	ACC	AAC	CGC	GGC	ATC	GTC	AAC	CAG	1390
Leu	Leu	Asn	Tyr	Ile	Gly	Gly	Thr	Thr	Asn	Arg	Gly	Ile	Val	Asn	Gln	
				450					455					460		
ACC	ACC	GAG	CAG	CTG	GTG	GAG	CAG	GTG	GAC	AAG	GAC	CTG	CGC	AAC	ATG	1438
Thr	Thr	Glu	Gln	Leu	Val	Glu	Gln	Val	Asp	Lys	Asp	Leu	Arg	Asn	Met	
				465					470					475		
GTC	ATC	AAG	CCC	GAC	GCG	CCC	AAG	CCC	CGT	GTG	GTG	GGC	GTG	CGC	GTG	1486
Val	Ile	Lys	Pro	Asp	Ala	Pro	Lys	Pro	Arg	Val	Val	Gly	Val	Arg	Val	
				480					485					490		
TGG	CCG	CGC	GCC	ATC	CCG	CAG	TTC	AAC	CTG	GGC	CAC	CTG	GAG	CAG	CTG	1534
Trp	Pro	Arg	Ala	Ile	Pro	Gln	Phe	Asn	Leu	Gly	His	Leu	Glu	Gln	Leu	
				500					505					510		
GAC	AAG	GCG	CGC	AAG	GCG	CTG	GAC	GCG	GCG	GGG	CTG	CAG	GGC	GTG	CAC	1582
Asp	Lys	Ala	Arg	Lys	Ala	Leu	Asp	Ala	Ala	Gly	Leu	Gln	Gly	Val	His	
				515					520					525		
CTG	GGG	GGC	AAC	TAC	GTC	AGC	GGT	GTG	GCC	CTG	GGC	AAG	GTG	GTG	GAG	1630
Leu	Gly	Gly	Asn	Tyr	Val	Ser	Gly	Val	Ala	Leu	Gly	Lys	Val	Val	Glu	
				530					535					540		
CAC	GGC	TAC	GAG	TCC	GCA	GCC	AAC	CTG	GCC	AAG	AGC	GTG	TCC	AAG	GCC	1678
His	Gly	Tyr	Glu	Ser	Ala	Ala	Asn	Leu	Ala	Lys	Ser	Val	Ser	Lys	Ala	
				545					550					555		
GCA	GTC	AAG	GCC	TAA	GCGGCTGCAG	CAGTAGCAGC	AGCAGCATCG	GGCTGTAGCT								1733
Ala	Val	Lys	Ala													
				560										563		
GGTAAATGCC	GCAGTGGCAC	CGGCAGCAGC	AATTGGCAAG	CACTTGGGGC	AAGCGGAGTG											1793
GAGGCGAGGG	GGGGGCTACC	ATTGGCGCTT	GCTGGGATGT	GTAGT												1838

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 <223> Designed oligonucleotide primer used for amplifying a DNA fragment containing a Chlamydomonas reinhardtii-derived PPO gene

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<223> Designed oligonucleotide primer used for constructing a vector for expressing a Chlamydomonas reinhardtii-derived PPO gene in Escherichia coli

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32

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a